

FIG. 1

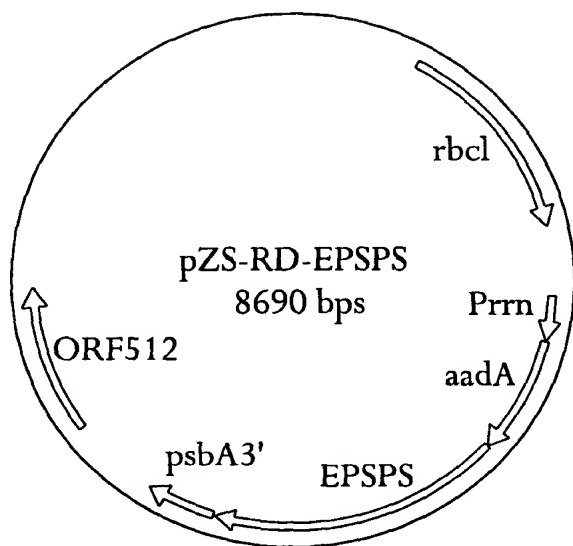


FIG. 2A

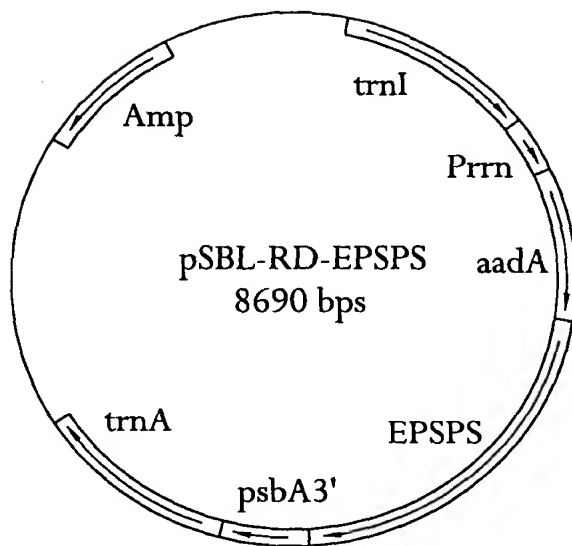


FIG. 2B

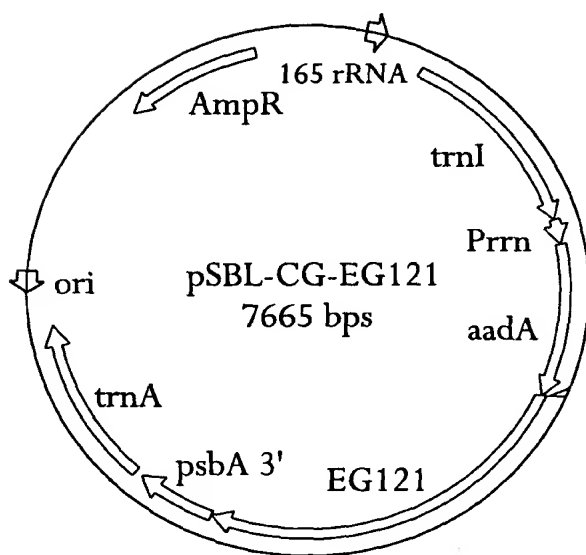


FIG. 3A

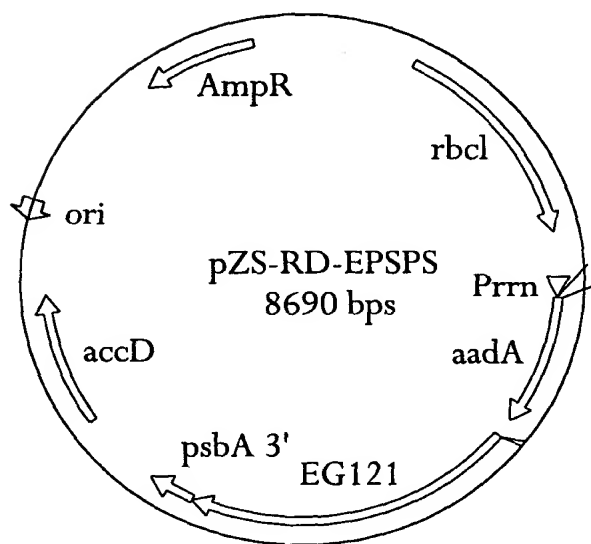
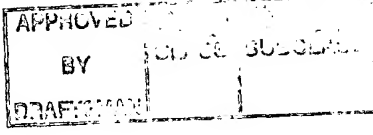


FIG. 3B

00079640-051598



Sequence alignment of 16S-23S rDNA spacer region from several crop species

```

*****
S GTACACACCGCCGTCACACTATGGGAGCTGGCCATGCC-GAAGTCGTTACC-TTAACCCGAAAG-AGGGGATGCCGAAGCAGGGCTAGTGCATGGAGT
T GTACACACCGCCGTCACACTATGGGAGCTGGCCATGCCGGAAGTCGTTACC-TTAACCCGAAAGGAGGGGATGCCGAAGCAGGGCTAGTGCATGGAGT
M GTACACACCGCCGTCACACTATGGAGCTGGCCAGGTTGAAGTCATTACCCCTAACCGTAAGGAGGGGATGCCTAAGGC TAGGCTTCCGAC TGGAGT

*****
S GAAGTCGTAAACAGGTAGCCGTACTGGAGGTGCGGCTGGATCACCCTCTTTTCAGGGAGAGCTAAATGCTTGT-----TGGGTAGTTTAGTTTGACACTGCTTCA
T GAAGTCGTAAACAGGTAGCCGTACTGGAGGTGCGGCTGGATCACCCTCTTTTCAGGGAGAGCTAAATGCTTGT-----TGGGTATTTTGGTTTGACACTGCTTCA
M GAAGTCGTAAACAGGTAGCCGTACTGGAGGTGCGGCTGGATCACCCTCTTTTCAGGGAGAGCTAAGCTTATGCTTATTTGGGTATTTTGGTTTGACACTGCTTCA

*****
S CACCC-----AAAAAGAGCGAGTTATGTCAGTCAAAATTTGGAGATGGAAGCTTCTTTTCGATGGTGAAGTAAGACTAAACTCATGAGCTTA
T CACCCCAAAAAAGAGCGAGCTACGTCAGTTAAACTTGGAGATGGAAGCTTCTTTTCGACGGTGAAGTAAGACCA-GCTCATGAGCTTA
M CGCCC-----AAAAAGAGCGAGCTACGTCAGCTAAACTTGGATATGGAAGCTTCTTTTCGTTT-----AGGGTGAAGTAAGACCAAGCTCATGAGCTTA

*****
S TTATCCTAGGTCGGACAAGTT-----GATAGGAGCTACTTTTTCATCA-CCCCCAT-----27bp-----ATGGGGGTGA AAAAGGAAAGAGAGGGATGGG
T TTATCCTAGGTCGGACAAGTT-----GATAGGACCCCTTTTACGTCCCCATGTTCCGCCCGTGTGGCGACATGGGGC-GAAAAAGGAAAGAGAGGGATGGG
M TTATCCTAGGTCGGACAAGTTAGTTGATAGTATAGGATCCCTTTTTCAGCTCCCCATGT-CCCCCGCTGTGGCGGCA TGGGATGTC AAAAGGAAAGGGATGGA-----

*****
S GTTCTCTTGCCTTTGGCATAGCGGGGCCCGGC-GGGAGGCCCGCACGACGGGCTATTAGTCAGTGGTAGAGCGGCCCTGATAATTGCGTCGTTGTG
T GTTCTCTCGCTTTGGCATAGCGGGGCCCGAGTGGAGGCTCGCACGCGGCTATTAGTCAGTGGTAGAGCGGCCCTGATAATTGCGTCGTTGTG
M GTTCTCTCGCTTTTGGGTAGCGGGCTCCCTTTTGGAGGC-CGCGCGACGGGCTATTAGTCAGTGGTAGAGCGGCCCTGATAATT-CGTCGTTGTG

```

FIG. 4A



```

*** * *****
S CCTGGACTGTAGGGC-TCTCAGCCACATGGATAGTTTAAATGTGCTCATCGGGCTTGACCTTGAGATGGGATCATCCAAGGCACATTAGCATGGCGTA
501 T CCTGGGCTGTAGGGCTCTCAGCCACATGGATAGTTCAATGTGCTCATCGGGCTTGACCTTGAGATGGGATCATCCAAGGCACATTAGCATGGCGTA
M CCTGGCTGTAGGGC-TCTCAGCCACATGGATAGTTCAATGTGCTCATCAGGGCTTGACCGGAGATGGGATCATCCAAGGCACATTAGCATGGCGTA

*** * *****
* ***** *
S CTTCCTCTGTTTGAAACCGGGTTTGAAACCAAC-----TTATCTCAGGAGGATAGATGGGGGATTGAGGTGAGATCCAAATGTAGATCCAACTTTCTCTTCAC
601 T CTCTCTCTGTTTGAAACCGGGTTTGAAACCAAC-----TCTCTCTCAGGAGGATAGATGGGGGATTGAGGTGAGATCCAAATGTAGATCCAACTTTCTCTTCAC
M CTCTCTCTGTTTGAAATCGGAGTTTGAAACCAACCAACAACTTCTCTCAGGAGGATAGATGGGGGATTGAGGTGAGATCCCAATGTAGATCGAACTTTCTCTTCAC

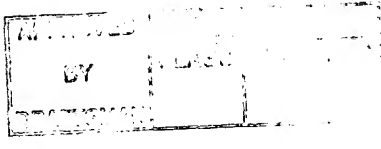
*** * *****
ori ends ↓
*****
S TCGTGGGATCCGGGCGATCCGGGGG ACCACCAGGCTCCCTCTCTCTCGAGAAATCATACATCCCTTATCAGTATATGGACAGTTATCTCTCGAGCACA
701 T TCGTGGGATCCGGGCGTCCGGGGG--ACCACCAGGCTCCCTCTCTCTCGAGAAATCCATACATCCCTTATCAGTATATGGACAGTTATCTCTCGAGCACA
M TCGTGGGATCCGGGCGTCCGGGGGACCACCGGGCTCCCTCTCTCTCGAGAAATCCATACATCCCTTATCAGTATATGGAGAGCTATCTCTCGAGCACA

*** * *****
S GGTTTAGGTTTGGCTCAAATGGAAAAAACGGAGCACCATAACAAGTATCTTCACAGACCAAGAACTACGAGATCGCCCTTTTCATTCTGGGGTGACGGTGGGATC
801 T GGTTTAGCAATGG-----GAAAAATAAAATGGAGCACCATAACAAGCCTATCTTCACAGACCAAGAACTACGAGATCGCCCTTTTCATTCTGGGGTGACGGAGGATC
M GGTTAGGTTCTGCTCAAATGGG--AAAAATGGAGCACCATAACAAGCCTATCTTCACAGACCAAGAACTACGAGATCGCCCTTTTCATTCTGGGGTGACGGAGGATC

*** * *****
S GTACCATTCGAGCC-----260bp-----TGGAGCAG-----GTTTGA AAAAGGATCTTAGAGTGTCTAGGGTTGTCTAGGAGGGTCTCATAATGCCCT
901 T GTACCATTCGAGCGTTTCTCTGACTCGAAATGGGAGCAG-----GTTTGA AAAAGGATCTTAGAGTGTCTAGGGTTGGGCCAGGAGGGTCTCTTACGCCCT
M GTACCATTCGAGCC--235bp--CTTGACTCGAAATGGGAGCAGCAGGTTTGA AAAAGGATCTTAGAGTGTCTAGGGTTGGGCCAGGAGGGTCTCTTACCCCT

```

FIG. 4B



```

** ***** * ***** * ***** * ***** * ***** * ***** * ***** * ***** * *****
S  TCCCTTTCTCTCATCGGAGTTATTCCCAAGACTTCCCATGGTAAAGAGA-AGGG-GGAACAAGCACACTTGGAGAGCCAGTACAACGGATAGTTG
1001 T  TCTTTTCTCTCATCGGAGTTATTACAAAGACTTCCCAAGGTAAGGAGA-AGGGGGAAACAAGCACACTTGGAGAGCCAGTACAACGGAGAGTTG
M  TCTTTTCTGCCCATCGGAGTTATTCCCAAGGACTTCCCGTGGTAAGGGGGAAGGGGGAAGCACACTTGAAGAGCCAGTACAACGGGGAGTTG

** ***** * ***** * ***** * ***** * ***** * ***** * ***** * ***** * *****
S  TATGCTGGTTCGGGAAGGATGAATCGCTCCGAAAGGAATCTATTGATTCCTCCCAATTGGTGGACGTAGGTGGATGATTACTTCACGGGGCGA
1101 T  TATGCTGGTTCGGGAAGGATGAATCGCTCCGAAAGGAATCTATTGATTCCTCCCAATTGGTGGACGTAGGTGGATGATTACTTCACGGGGCGA
M  TATGCTGGTTCGGGAAGGATGGATCGCTCCGAAAGGAGTCTATTGATTCCTCCCAATTGGTGGATCGTAGGGGGGATGATTACTTCACGGGGCGA

                                     ↓ site of foreign gene insertion
** ***** * ***** * ***** * ***** * ***** * ***** * ***** * ***** * *****
S  GGTCTCTGGTTCAGTCCAGATGGCCAGCTCCGTCAGGGAAGAAATAGAAAACGTACTTGACTCCTTCATGCAATGCTCCACTCGGCTCGGGGGG-ATA
1201 T  GGTCTCTGGTTCAGTCCAGATGGCCAGCTCCGTCAGGGAAGAAATAGAAAACGTACTTGACTCCTTCATGCAATGCTCCACTCGGCTCGGGGGG-ATA
M  GGTCTCTGGTTCAGTCCAGGATGGCCAGCTCCG-CAGGGGAAGAAATAGAAAACGTACTTGACTCCTTCATGCAATGCTCCACTCGGCTCGGGGGGATA

** ***** * ***** * ***** * ***** * ***** * ***** * ***** * ***** * *****
S  TAGCTCAGTTGGTAGAGCTCCGCTCTTGCAATTGGGTGCTTGGCATACGGGTGGATGCTCTAATTGCTAGGGGGTAATGATAGTATCTTGTACCTGAA
1301 T  TAGCTCAGTTGGTAGAGCTCCGCTCTTGCAATTGGGTGCTTGGCATACGGGTGGATGCTCTAATTGCTAGGGGGTAATGATAGTATCTTGTACCTGAA
M  TAGCTCAGTTGGTAGAGCTCCGCTCTTGCAATTGGGTGCTTGGCATACGGGTGGATGCTCTAATTGCTAGGGGGTAATGATAGTATCTTGTACCTGAA

** ***** * ***** * ***** * ***** * ***** * ***** * ***** * ***** * *****
S  CCGGTGGCTCACITTTTCTAAGTAAATGGGAAGAGGACCGGAACATGCCACTGAAGACTCTACTGAGACAAA--GACGGGCTGTCAAGAACGTAGAGGAGG
1401 T  CCGGTGGCTCACITTTTCTAAGTAAATGGGAAGAGGACCGGAACATGCCACTGAAGACTCTACTGAGACAAA--GATGGGCTGTCAAGAACGTAGAGGAGG
M  CCGGTGGCTCACITTTTCTAAGTAAATGGGAAGAGGACTGAACATGCCACTGAAGACTCTACTGAGACAAAAGATGGGCTGTCAAAAGGTAGAGGAGG

```

FIG. 4C

S TAGGATGGGCAGTTGGTCAGATCTAGTATGGATCGTACATGGACGGTAGTTGGAGTCGGTGGCTCCTAGGGTTTCCTCATTTGGGATC-CTGGGGAAG
1501 T TAGGATGGGCAGTTGGTCAGATCTAGTATGGATCGTACATGGACGGTAGTTGGAGTCGGGCGCTCCAGGGTCCCTCATCTGAGATCTCTGGGGAAG
M TAGGATGGGCAGTTGGTCAGATCTAGTATGGATCGTACATGGACGGTAGTTGGAGTCGGGCGCTCCTAGGGTTCCTCATCTGGGATCCCTGGGGAAG

S AGGATCAAGCTGGCCCTTGGGAACAGCTTGATGCACATATCTCCCTCAACCCTTTACGCCGAAATGTGGC-----AAAGGAAAAAGAAATCCATGGACCGA
1601 T AGGATCAAGTTGGCCCTTGGGAACAGCTTGATGCACATATCTCCCTCAACCCTTTACGCCGAAATGTGGC-----AAAGGAAAAAGAAATCCATGGACCGA
M AGGATCAAGTTGGCCCTTGGGAATAGCTTGATGCACATATCTCCCTCAACCCTTTACGCCGAAATGTGGC-----AAAGGAAAGGAAAAATCCATGGACCGA

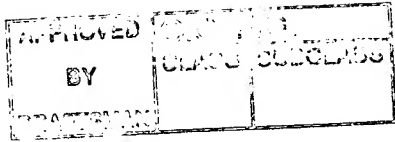
S CCCCATCGTCTCCACCCCGTAGGAACACGAGATCACCCCAAGGAACGCCCTTCGGCATCCAGGGGTCCGGACCGACCATAGAACCTGTTCAAAAAGCG
1701 T CCCCATCATCTCCACCCCGTAGGAACACGAGATCACCCCAAGGAACGCCCTTCGGCATCCAGGGGTCCGGACCGACCATAGAACCTGTTCAAATAAGTG
M CCCCATGTCTCCACCCCGTAGGAACACGAGATCACCCCAAGGAGTTCGTCTCAATGGGGGTCTATCGGACCGACCATAG-ATCCTGTTCAAATAAGTG

S GAACGCATTAGCTATCCGCTCTCAGGTGGACAGTAAGGGTCGGAGAGGGCAATCATTCTTA-112bpTTAGAATGGGATTCCAACTCAGCACCTTT---
1801 T GAACGCATTAGCTATCCGCTCTCAGGTGGGCGAGTCAGGGTCGGAGAGGGCAATGACTATTCTTA-----GTTAGAATGGGATTCCAACTCAGCACCTTTGA
M GAACACAATAGCCGTCGCTCTCCGGTTGGGCGAGTAAGGGTCGGAGAGGGCAATCATTCTTA-103bp-TTAGAATGGGATTCCAACTCAGCACCTTTTGT

S --TGAGATTTTGAGAAGAGTTGCTCTTTGGAGAGCACAGTACGATGAAAGTTGTAGCTGTGTCGGGGGGGAGTTATTGTCATCGTTGGCTCTAIGGT
1901 T G-TGAGATTTTGAGAAGAGTTGCTCTTTGGAGAGCACAGTACGATGAAAGTTGTAGCTGTGTCGGGGGGGAGTTATTGTCATCGTTGGCTCTAIGGT
M TTTGGGATTTTGAGAAGAGTTGCTCTTTGGAGAGCACAGTACGATGAAAGTTGTAGCTGTGTCGGGGGGGAGTTATTGCTATCGTTGCTCTAIGGT

FIG. 4D

365F50" 04964060



```

*** * *****
S AGAATCAGTCGGG---CCTGAGAGGCGGTGGTTACCTGTGGCGGATGTCAGCGGTTCGAGTCCGCTTATCTCCAACTCGTGAACCTAGTCGATACAAA
2001 T AGAATCAGTCGGG-GACCTGAGAGGCGGTGGTTACCTGCGGGGATGTCAGCGGTTCGAGTCCGCTTATCTCCAACTCGTGAACCTAGTCGATACAAA
M AGAACCCTCGGGAGGCGCTGAGAGGCGGTGGTTACCTGTGGCGGATGTCAGCGGTTCGAGTCCGCTTATCTCCAGCCGCTGAACCTAGTCGATAC---

```

S GCTA

2101 T GCTT

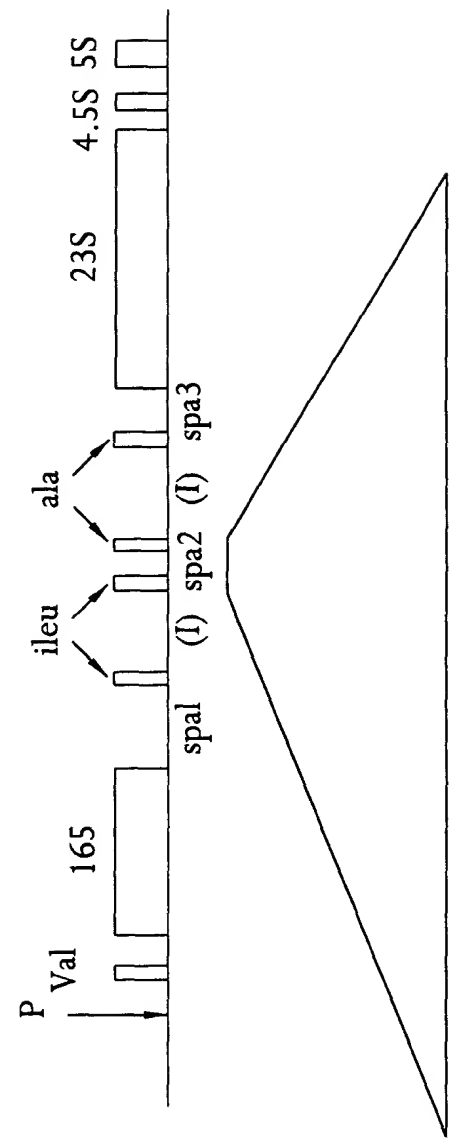
M ----

* indicates homology
- indicates gaps in the sequence compared to each other sequences
Nucleotide number corresponds to tobacco sequences only
S-soybean, T-tobacco, M-maize

FIG. 4E

065750" 04962060

GENE SEQUENCE OF rRHA CODING REGIONS IN PLASTID DNA FROM HIGHER PLANTS



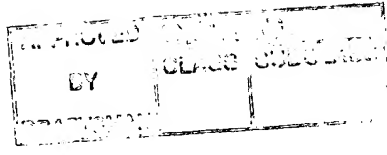
SEQUENCE ALIGNMENT OF SPACER-2 (64 bp) REGION FROM SEVERAL CROP SPECIES WITH TOBACCO

EPIFAGUS (90 %)	GCTGGCGCTA-GGAAAAAATATAAAAGCATCTGATTACTTTCATGCAIGCT
TOBACCD (+) ---	GCTGGCCAGGGAAGAAATAGAAAGCATCTGACTACTTTCATGCAIGCTCCA-CTTGGGCTCGG

HELIANTHUS(96 %)	CGTGGCCAGGGAAAAAGAAATAGAAAGCGCTGACTCCTTCATGCAIGCTCCA-CTTGGGCTCGG
DENOTHERA (96 %)	GCTGGCAAGGAAAAAGAAATAGAAAGCATCTGACTCCTTCATGCAIGCTCCA-CTTGGGCTCGG
ALNUS (95 %)	GCTGGCCCAAGTAAAAAGAAATAGAAAGCATCTGACTCCTTCATGCAIGCTCCA-CTTGGGCTCGG
RICE (95 %)	GCTGGCCAGGGAAGAAATAGAAAGCATCTGACTCCTTCATGCAIGCTCCA-CTTGGGCTCGG
MAIZE (94 %)	GCTGGG-CAGGGAAAAAGAAATAGAAAGCATCTGACTCCTTCATGCAIGCTCCA-CTTGGGCTCGG
SOYBEAN (84 %)	GCTGGCTCAAGGAAAAAGAAATAGAAAGCATCTGACTCCTTCATGCAIGCTCCA-CTCGGGCTCGG

FIG. 4F

EST50" 04962050



PEA	(89	%)	GCTGGCCCAAGGAAAAGACTAAAGACGGATTGACTCCTTCATGCTCCAACTTGGCTCGG
SPINACH	(89	%)	ACTGGCCCAAGAA <u>T</u> AAGAA <u>T</u> CGAAGAAGCGTCTGACTCCTTCATGCTCCCA-CTTGGCTCGG

/ \
CGCCAGGGAA

T0BACCO	(-)	---	CCGAGCCCAAGTGGAGCATGCATGAAGTAGTCAGATGCTTCTTCTATTCTTTTCCCTGGCGCAGC
CUSCUTA	(96	%)	CCGAGCCCAAGTGGAGCATGCATGAAGTAGTCAGATACCTCTTCGATTCTTTTCCCTGGCGCAGC

FIG. 4G

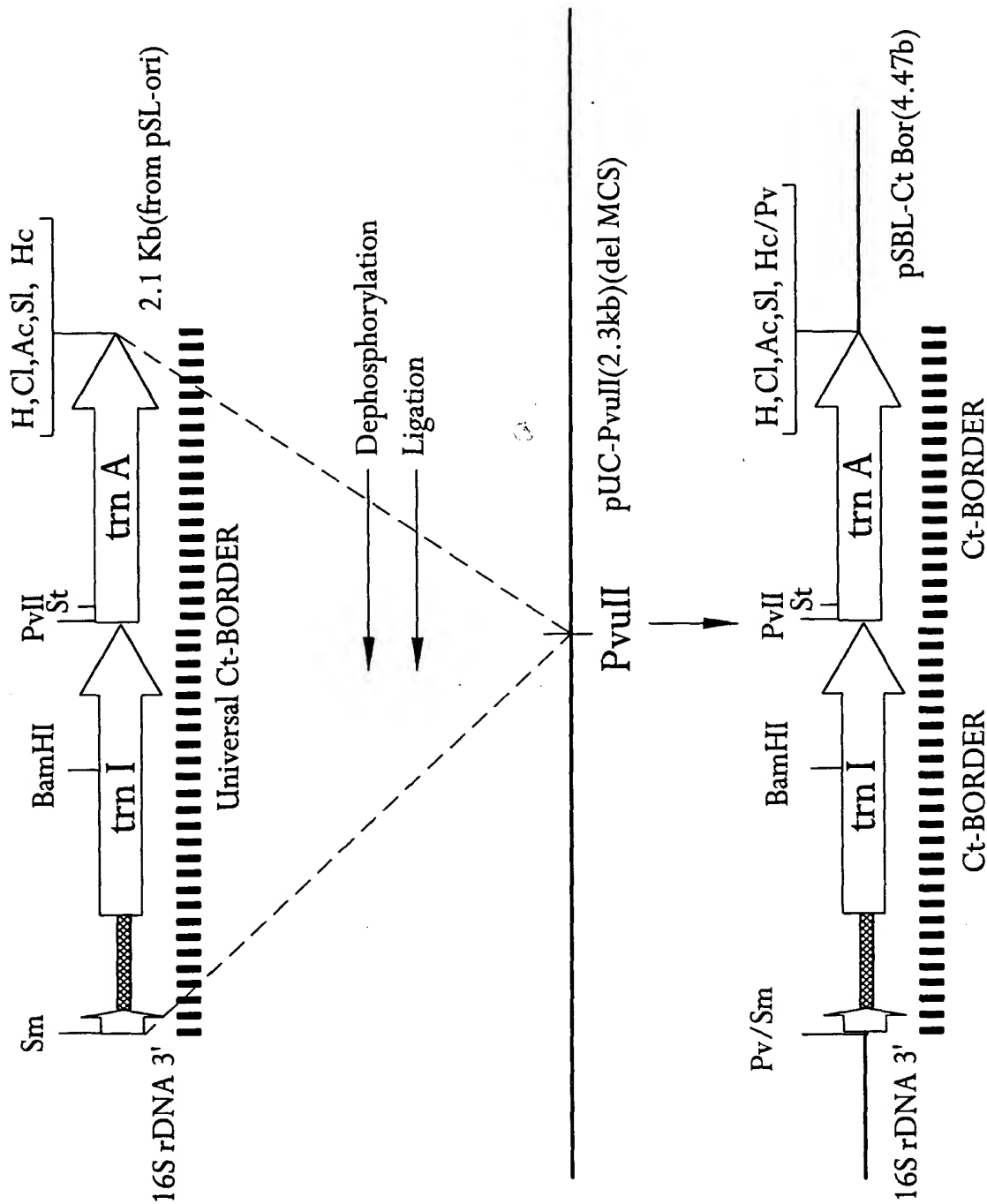


FIG. 5

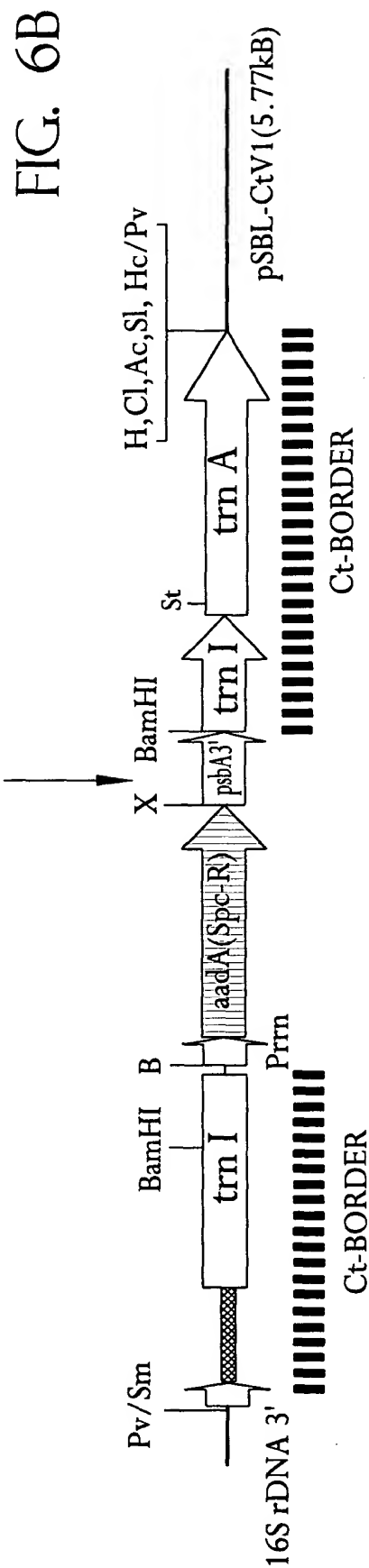
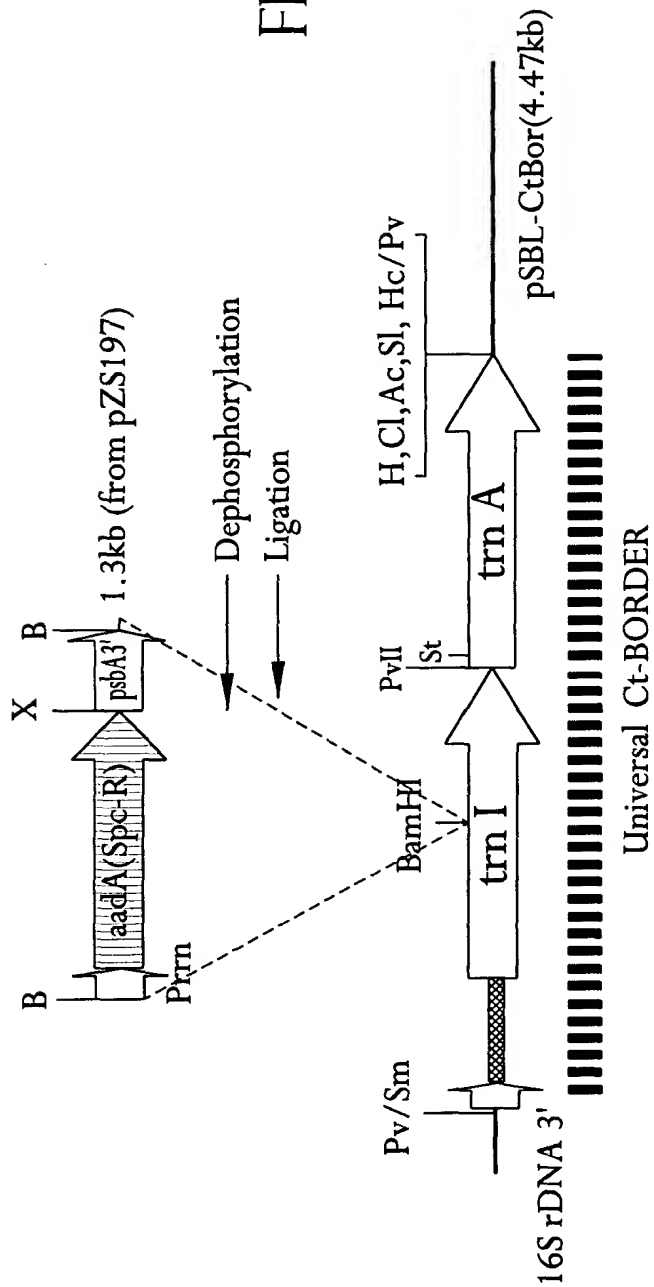


FIG. 6C

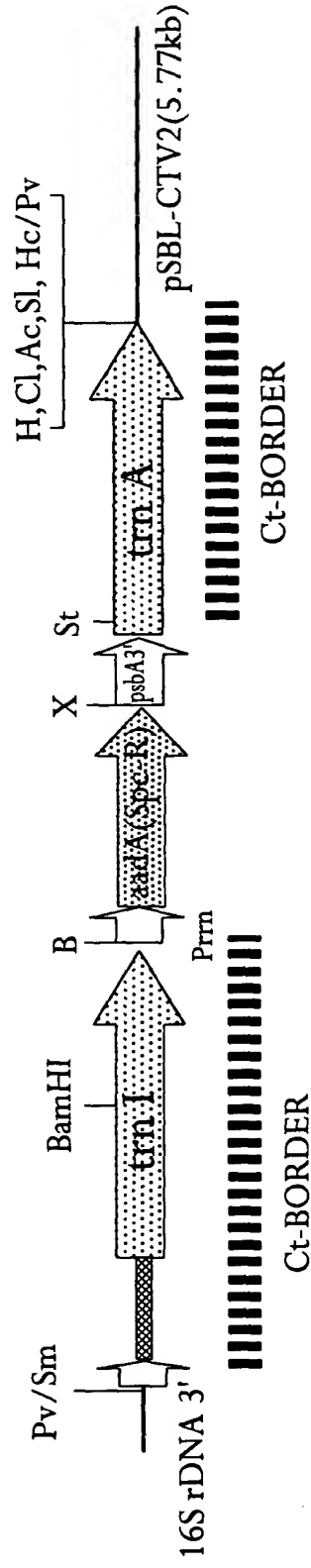


FIG. 7A

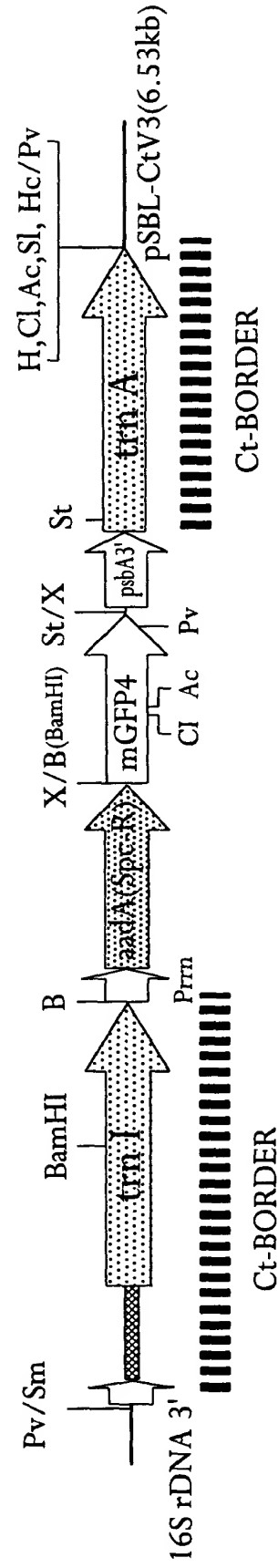


FIG. 7B

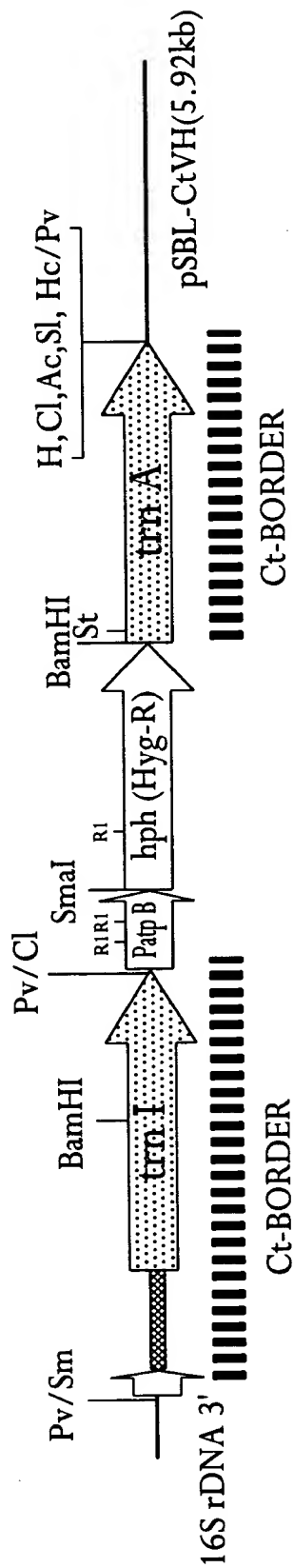


FIG. 7C

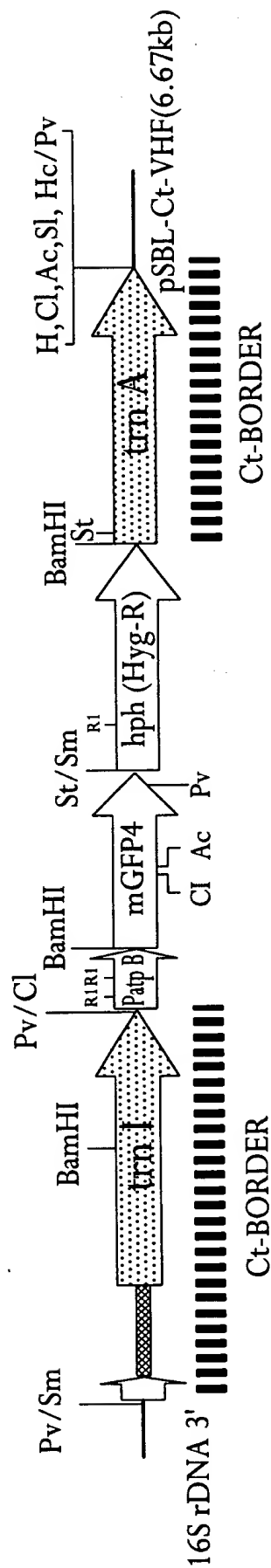


FIG. 7D

7. APPROVED	DATE	BY	CLASS	SUBCLASS

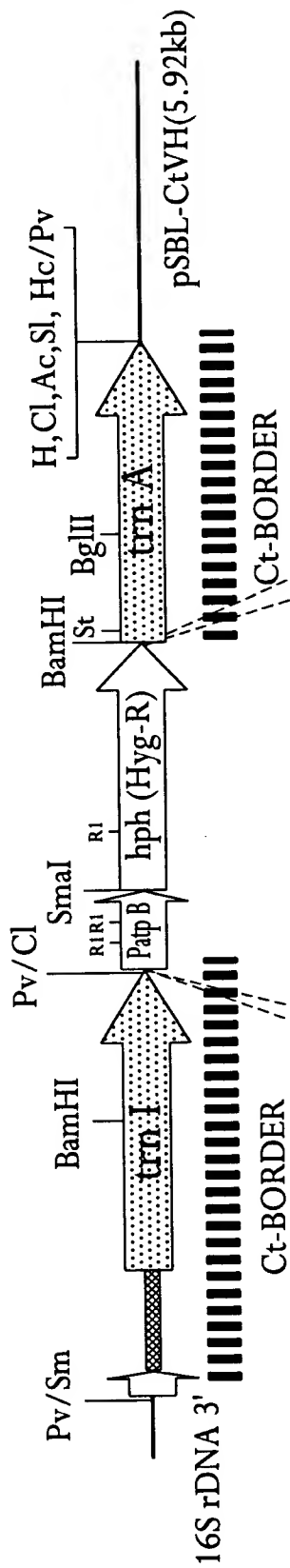


FIG. 8A

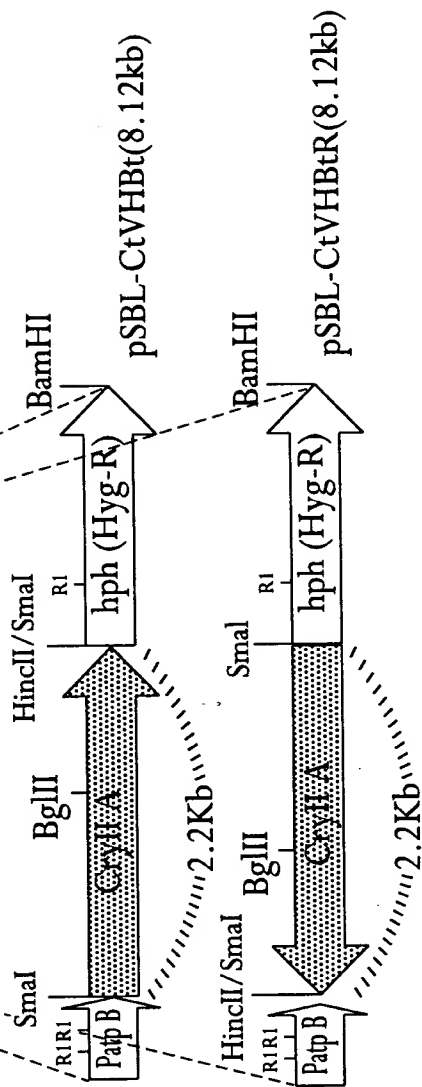


FIG. 8B



FIG. 9

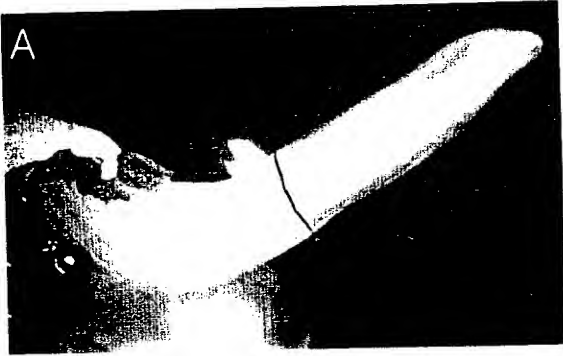


FIG. 10A

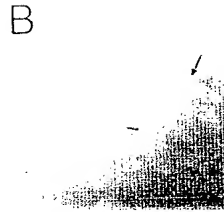


FIG. 10B



FIG. 10C



FIG. 10D



FIG. 10E



FIG. 10F

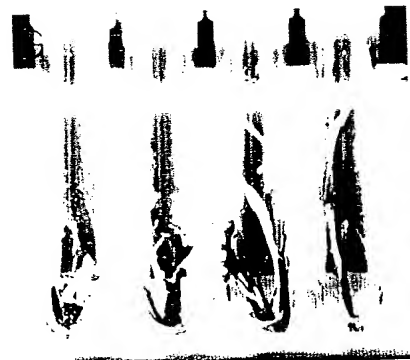


FIG. 10G



FIG. 11



FIG. 12A

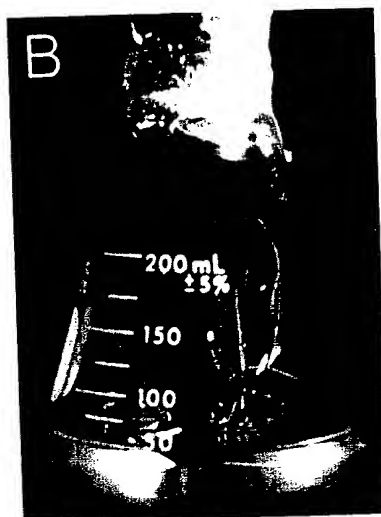


FIG. 12B



FIG. 12C

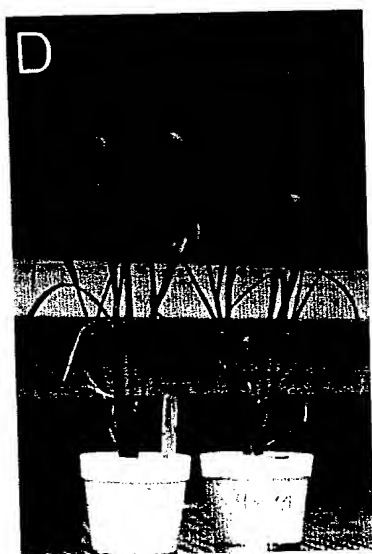


FIG. 12D

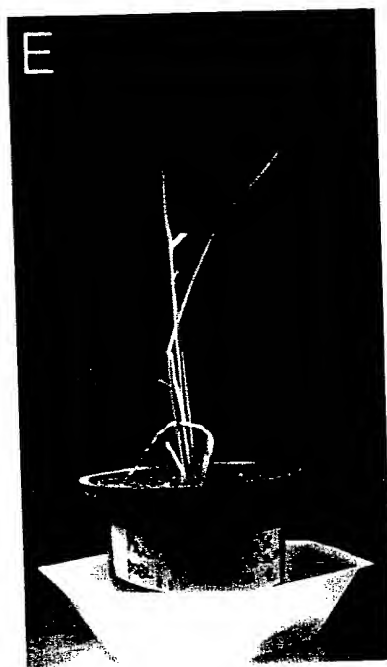


FIG. 12E

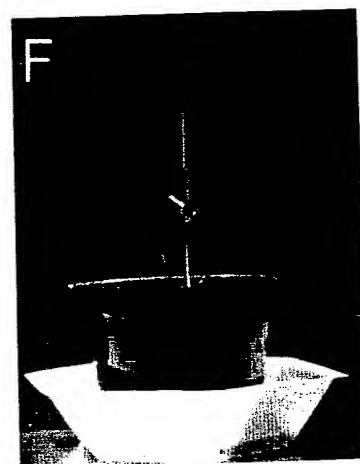


FIG. 12F

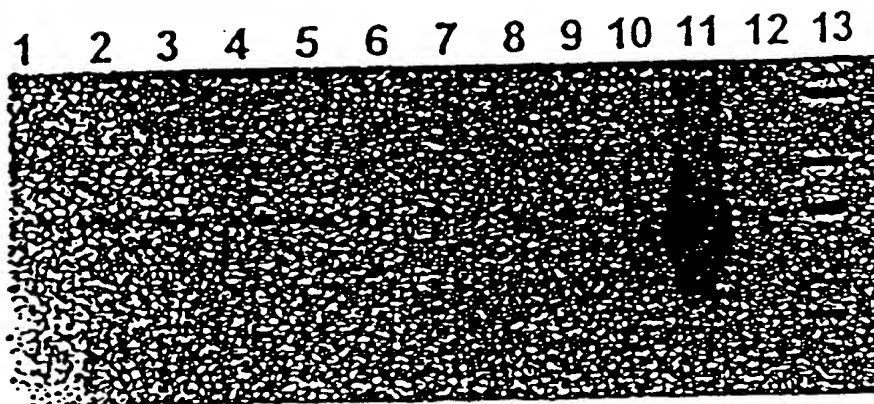


FIG. 13A

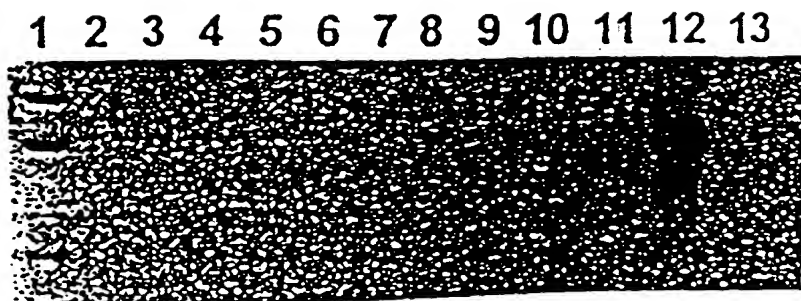


FIG. 13B

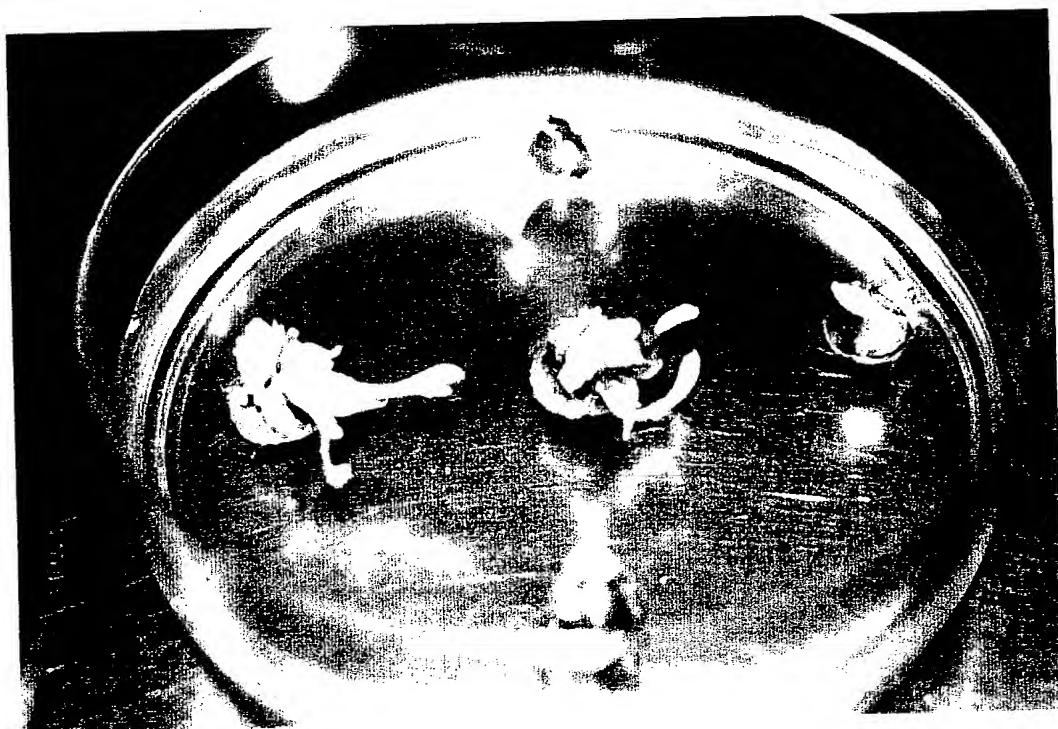


FIG. 14



FIG. 15



FIG. 16



FIG. 17

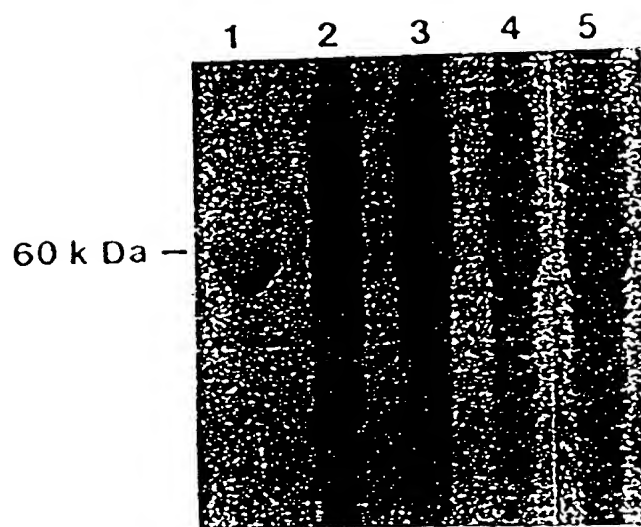


FIG. 18

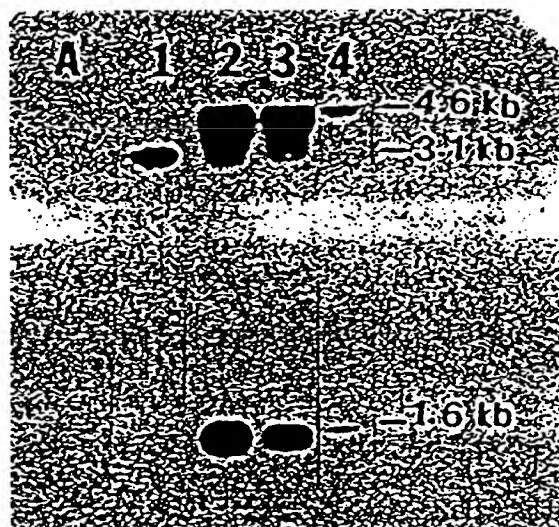


FIG. 19A

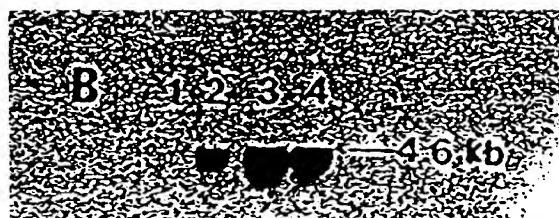


FIG. 19B

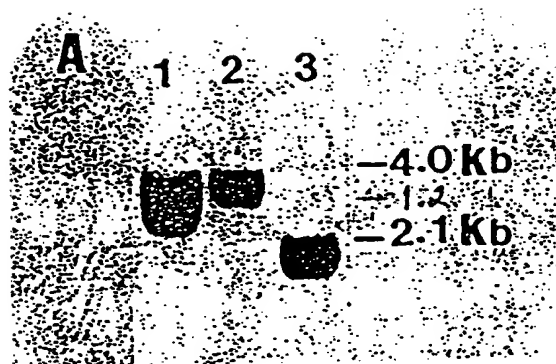


FIG. 20A

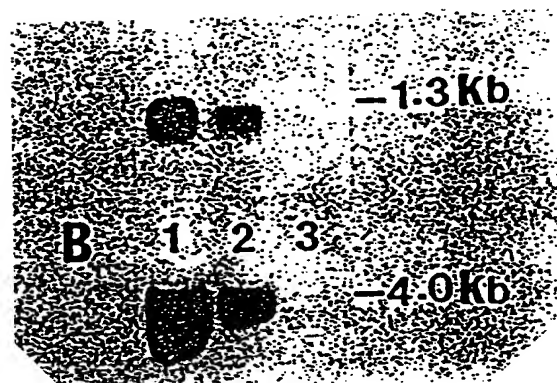


FIG. 20B

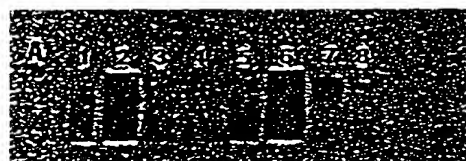


FIG. 21A

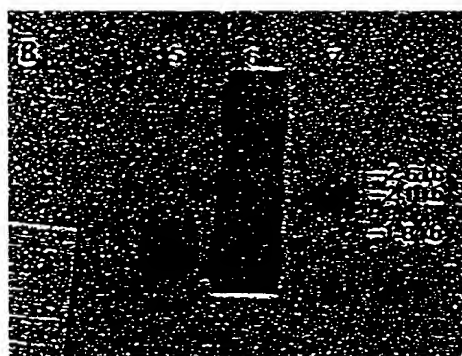


FIG. 21B

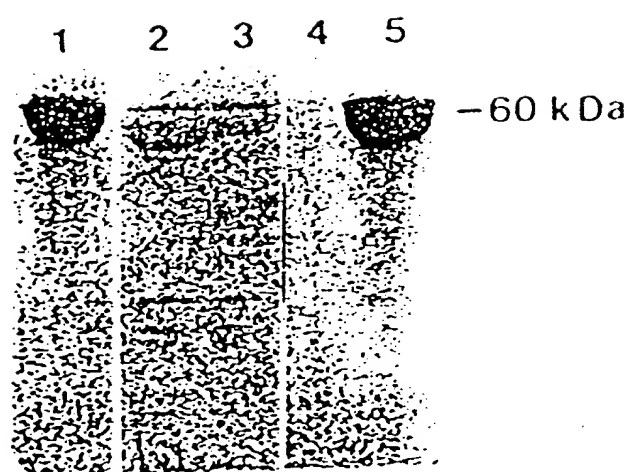


FIG. 22

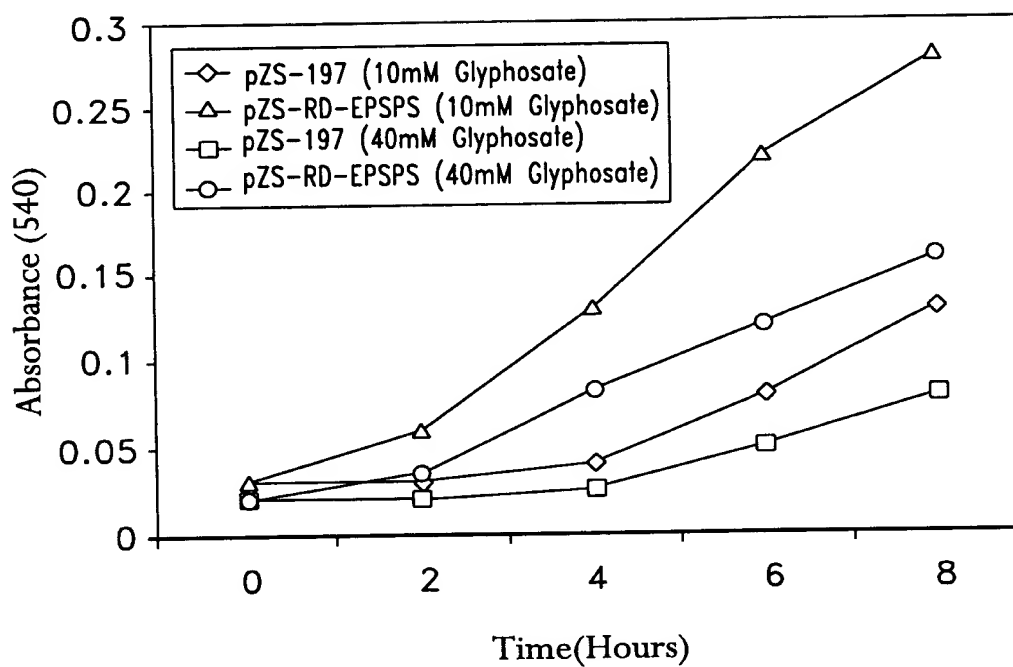


FIG. 23A

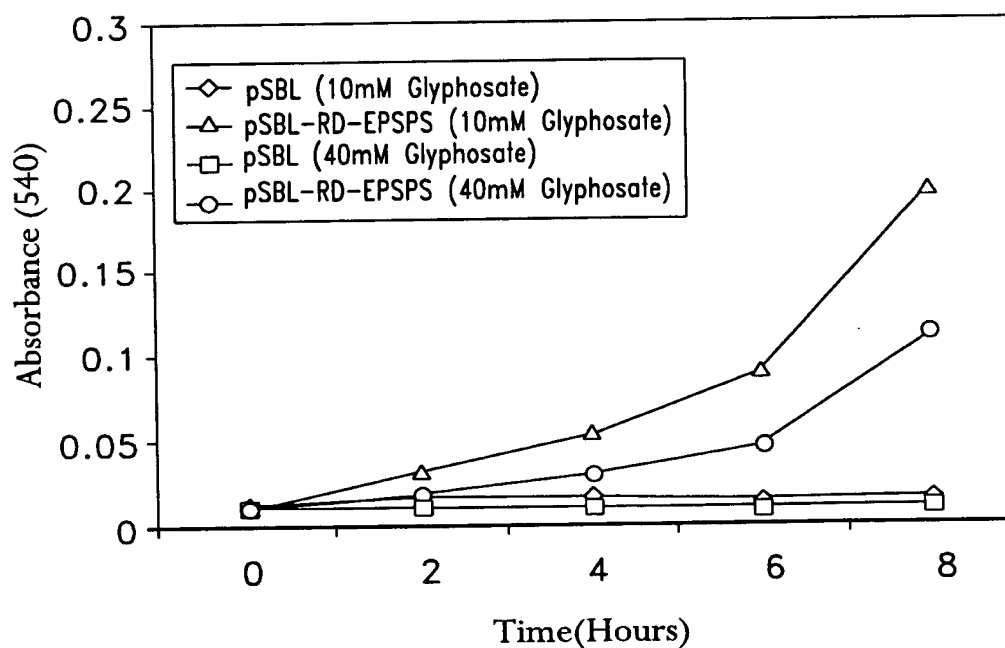


FIG. 23B

365T50" 04962060

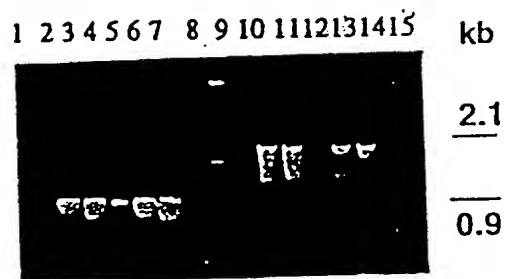


FIG. 24A

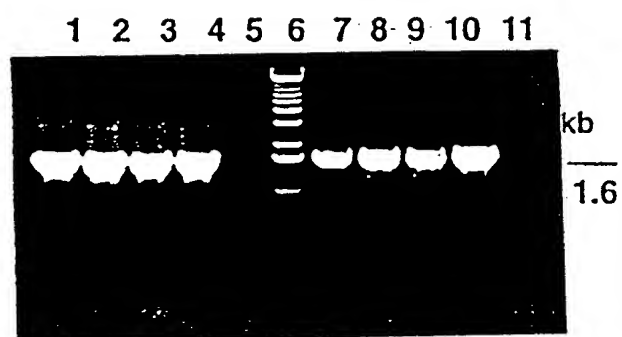


FIG. 24B

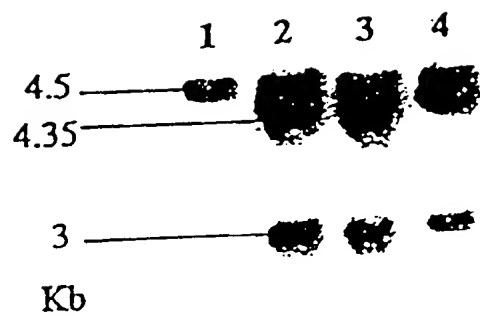


FIG. 25A

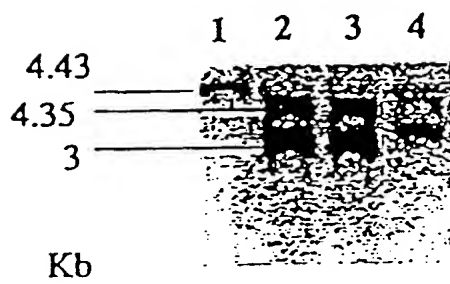


FIG. 25B

07/07/2006

865T50" 04962060

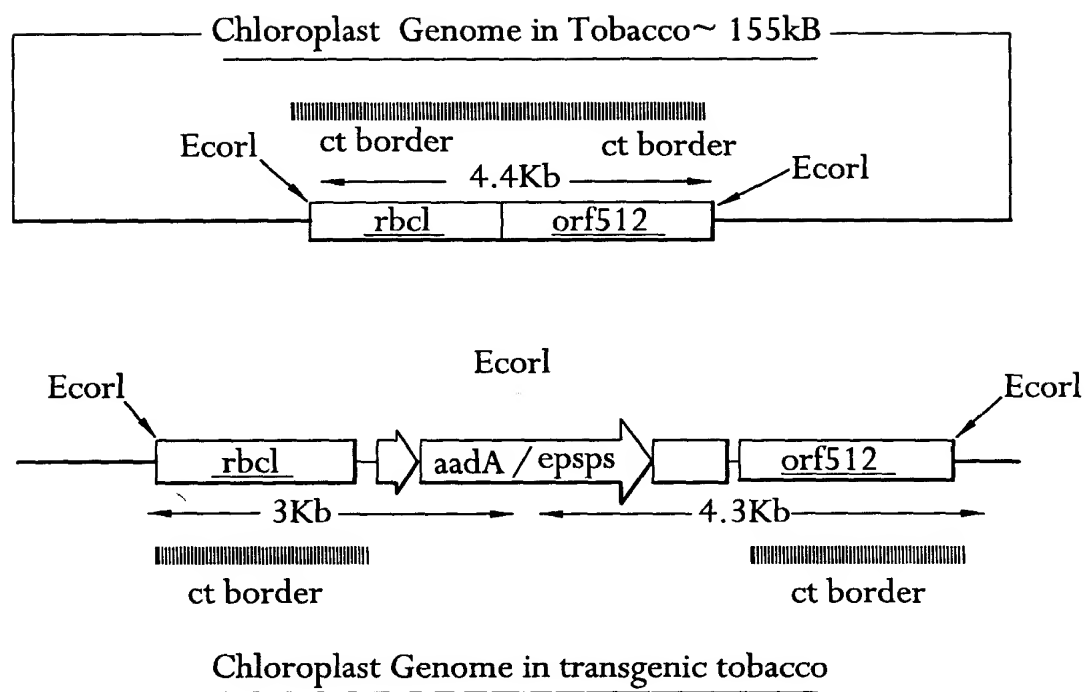


FIG. 25C

A

B



FIG. 26A

FIG. 26B

A

B



FIG. 27A

FIG. 27B

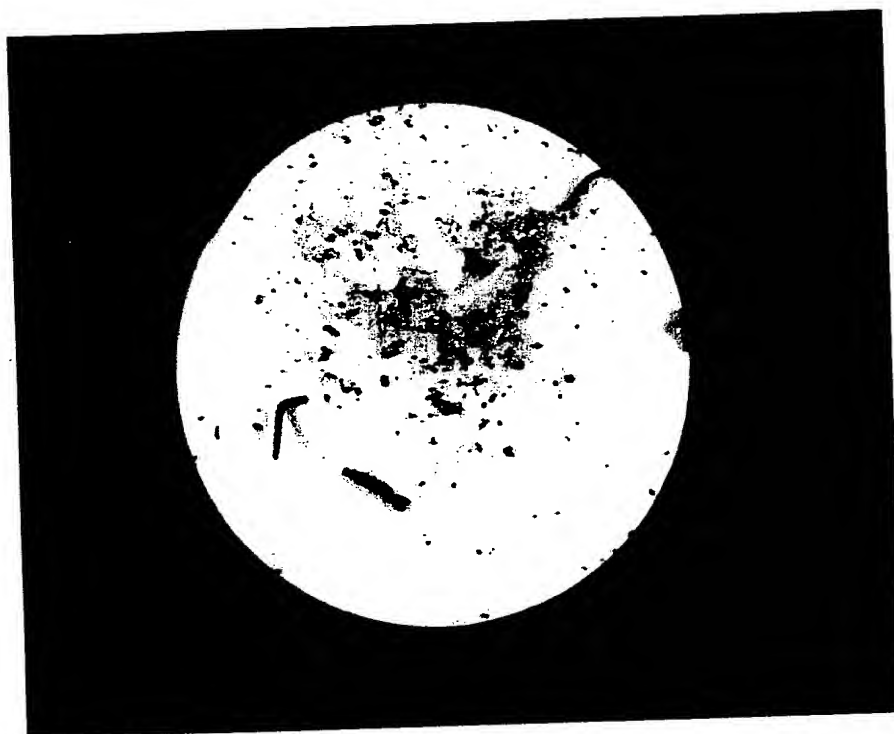


FIG. 28A

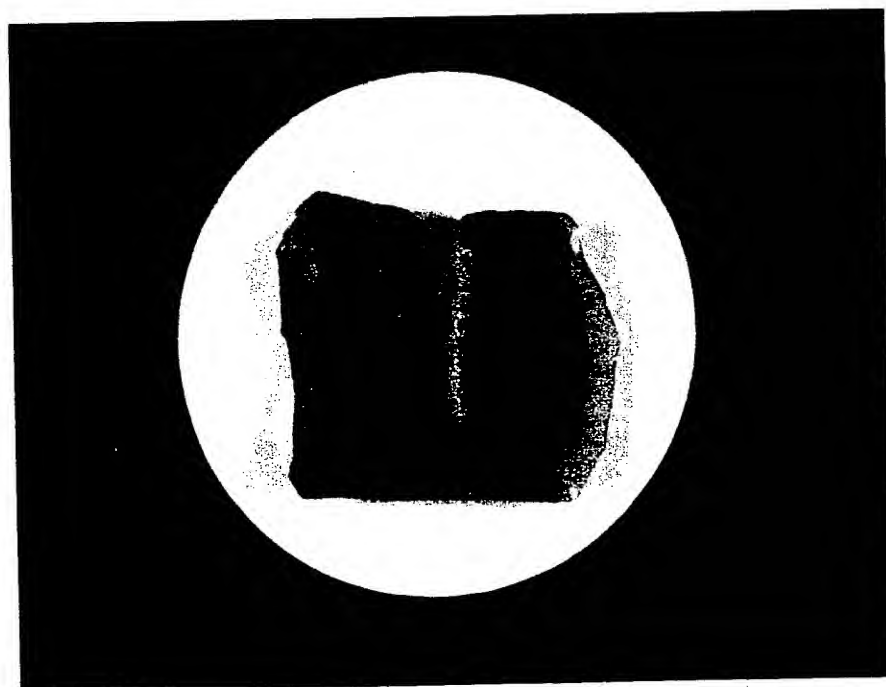


FIG. 28B

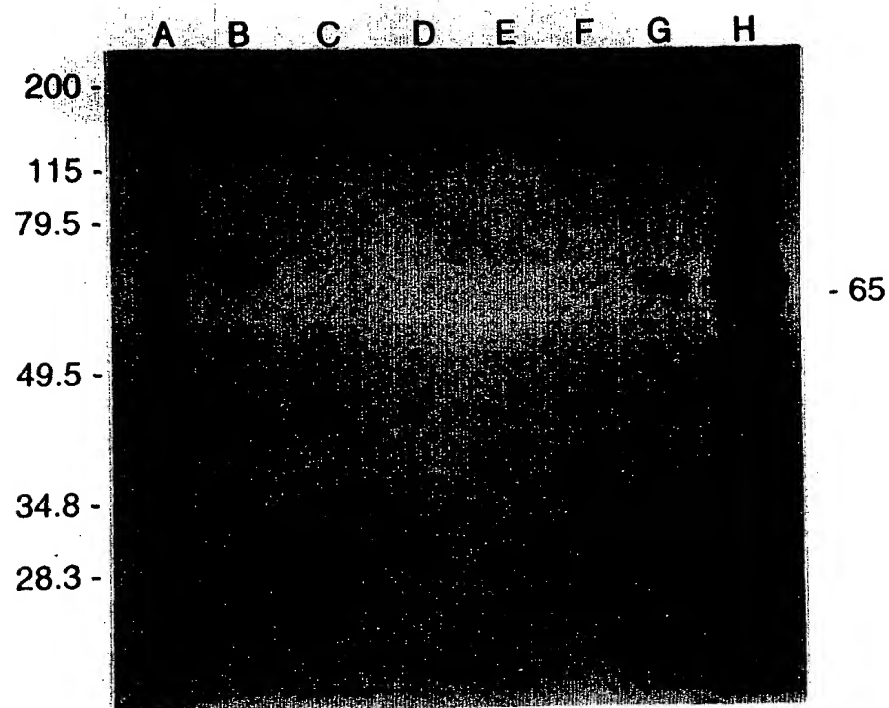


FIG. 29